

1/16

Figure 1

IM2169

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M978

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      10      20      30      40      50      60
CLGGGGSFDLDSVDTEAPRPAPKYQDVSSEKPAQKDQGGYGFMRLKRRNWYPGAE--ESEVKLNESDW
=====
CLGGGGTFDLDSVDTEAPRPAPKYQDVSSEKPAQKDQGGYGFMRLKRRNWHFQANPKEDIKLSNDW
      10      20      30      40      50      60      70

      70      80      90     100     110     120     130
EATGLPTKPKELPKRQKSVIEKVETDGDSDIYSSPYLTPSNHQNGSAGNGVNPKNQATGHENFQYVYSG
=====
EATGLPGNPKNLPERQKSVIEKVKTGSDSNYSSPYLTQSNHONGSA-N---QPKNEVKDYKEFKYVYSG
      80      90     100     110     120     130

      150     160     170     180     190     200
WFKYKHAASE--KDFS-NKKIKSGDDGYIFYHGEKPSRQLPASGKVYKGVWHFVTDTKKGQDFREIIQPS
=====
WFKYKHALEIIKENNLKGAKSDDGYIFYHGEKPSRQLPVSGEVYKGVWHFVTDTKQGQKFNDILGTS
      140     150     160     170     180     190     200

      210     220     230     240     250     260     270
KKQGD RYSGFSGDGSEEYSNKNESTLKDDHEGYGFTSNLEVD FGNKKLTGKLI RNNASLNNNTNNDKHTT
=====
KKQGD RYSGFPGDDGEEYSNKNEATLQGSQEGYGFTSNLKVD FNNKKLTGELI RNN-RVTNATANDKYTT
      210     220     230     240     250     260     270

      280     290     300     310     320     330     340
QYYSLEAQITGNRFNGTATATDKKEN-ETKLHPFVSDSSSLSGGFFGPQGEELGFRFLSDDQKVAVVGSA
=====
QYYSLEAQVTGNRFNGKATATDKPGTGETKQHPFVSDSSSLSGGFFGPKEELGFRFLSNDQKVAVVGSA
      280     290     300     310     320     330     340

      350     360     370     380     390     400     410
KTKDKLENG--AAASGSTGAAASGGAAGTSSSENSKLTTVLDAVELTLNDKKIKNLDNFSNAAQLVVDGIM
=====
KTQDKAANGNTAAASGGTDAAASNGAAGTSSSENSKLTTVLDAVELTLNDKKIKNLDNFSNAAQLVVDGIM
      350     360     370     380     390     400     410

      420     430     440     450     460     470
IPLLPKDSESGNTQADKKGK---NG--G-TEFTRKFEHTPESDKKD--AQAGTQ-TNGAQTASNTAGDTNG
=====
IPLLPESESQADKKGKNGKNGGTDFTYKTTYTPKNDDKDTKAQTGAAGSSGAQTDLGKADVNGG
      420     430     440     450     460     470     480

      480     490     500     510     520     530     540
K--TKTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGGNSSQADAKTEQVEQSMFLQGERTDEKEIPTDQN
=====
KAETKTYEVEVCCSNLNYLKYGMLTRKNSKSAMQAGGNSSQADAKTEQVEQSMFLQGERTDEKEIPNDQN
      490     500     510     520     530     540     550
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      550      560      570      580      590      600      610
VVYRGSWYGHIANGTSGNSASDKEGGNRAEFTVNFADKKITGKLTAENRQAQTFTIEGMIQGNFGFTA
=====
VVYRGSWYGHIASSTSGNSASNATSGNRAEFTVNFDTKKINGTLTAENRQEATFTIDGKIEGNFGSFTA
      560      570      580      590      600      610      620

      620      630      640      650      660      670      680
KTAESGFDLDQKNTRTPKAYITDAKVGGFYGPKAELGGWFAYPGDKQTEKATATSSDGNSSASSATVV
=====
KTADLGFDLDQSNTTGTTPKAYITDAKVGGFYGPKAELGGWFAYPGDKQTEKATVASGDGNSSASSATVV
      630      640      650      660      670      680      690

      690
FGAKRQQPVQ
=====
FGAKRQQPVQ
      700
```

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Figure 2

IM2169

6940

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      10      20      30      40      50      60      70
CLGGGGSFDLDSVDTEAPRPAPKYQDVSSEKPAQKQDGGYGFMRLKRRNWYPGAEESEVKLNESDWEA
=====
CLGGGGTFDLDSVDTEAPRPDPKYQDVSSEKPAQKQDGGYGFMRLKRRNWYSAAKEDEVKLNESDWET
      10      20      30      40      50      60      70

      80      90     100     110     120     130
TGLPTKPKELPKRQKSVIEKVETD-GDSDIYSSPYLTPSNHQNGSAGNGVNQPKNQATGHENFQYVYSGW
=====
TGLPTEPKKLPLKQESVISKVQANNGDNNIYTSPLYLTQSNHQNSSINGGANLPKNEVTNYKDFKYVYSGW
      80      90     100     110     120     130     140

      150     160     170     180     190     200
FYKHAASE--KDFSNNK-IKSGDDGYIFYHGKPSRQLPASGKVIYKGVWHFVTDTKKGQDFREIIQPSK
=====
FYKHAKNEIIRENSSIKGAKNGDDGYIFYHGKPSRQLPASGTVTYKGVWHFATDVKKSONFRDIIQPSK
      150     160     170     180     190     200     210

      210     220     230     240     250     260     270
KQGDYSGFSGDGGSEESYNNKNESTLKDDHEGYGFTSNLEVDFGNKKLTGKLI RNNASLNNNTNNDKHTTQ
=====
KQGDYSGFSGDDDEQYSNNKNESTLKDDHEGYGFTSNLEVDFGSKKLTGKLI RN--RVTNAPTNDKYTTQ
      220     230     240     250     260     270

      280     290     300     310     320     330     340
YYSLDAQITGNRFRNGTATATDKKENE-TKLHPFVSDSSSLSGGFFGPQGEELGFRFLSDDQKVAVVGS AK
=====
YYSLDAQITGNRFRNGKAIRTDKPD TGKTLHPFVSDSSSLSGGFFGPKEELGFRFLSDDKKVAVVGS AK
      290     300     310     320     330     340

      350     360     370     380     390     400     410
TKDKLENGAAASGSTGAAASGGAAGTSSSENSKLTTVLDAVELTLNDKKIKNLDNFSNAAQLVVDGIM I PL
=====
TKDKTENGAVASGGTDAAASNGAAGTSSSENSKLTTVLDAVELKLGDKEVQKLDNFSNAAQLVVDGIM I PL
      360     370     380     390     400     410

      420     430     440     450     460     470     480
LPKDESGNTQADKGKNGGTEFTTRKFEHTPESDKKDAQAGTQTNGAQTASNTAGDTNGKTKTYEVEVCCS
=====
LPEASESGNNQANQGTNGGTAFTTRKFDHTPESDKKDAQAGTQTNGAQTASNTAGDTNGKTKTYEVEVCCS
      430     440     450     460     470     480

      490     500     510     520     530     540     550
NLNYLKYGMLTRKNSKSAMQAGGNSSQADAKTEQVEQSMFLQGERTDEKEIPTDQNVVYRGSWYGH I ANG
=====
NLNYLKYGMLTRKNSKSAMQAGESSSQADAKTEQVEQSMFLQGERTDEKEIPSEQNIVYRGSWYGY I ANG
      500     510     520     530     540     550

      560     570     580     590     600     610     620
--TSWSGNASDKEGGNRAEFTVNFADKKITGKLTAE NRQAQTFTIEGMIQGNFGEGTAKTAESGF DLDQK
=====
KSTWSGNASNATSGNRAEFTVNFADKKITGTLTADNRQEATFTIDGNIKDNFGEGTAKTAESGF DLDQS
      570     580     590     600     610     620
```

630	640	650	660	670	680	690
NTTTRTPKAYITDAKVKGFFYGPKAEELGGWFAYPGDKQTEKATATSSDGNSASSATVVFGAKRQQPVQ						
=====						
NTTTRTPKAYITDAKVQGGFYGPKEELGGWFAYPGDKQT-KN-ATNASGNS-S-ATVVFGAKRQQPVR						
640	650	660	670	680	690	

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Figure 3

IM2169

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S3032

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      10      20      30      40      50      60
CLGGGG-SFDLDSVDTEAPRPAPKYQDVSSEKPAQKQDQGGYGAMRLKRRNWYPGAEESEVKLNESDWE
=====
CLGGGGGSFDLDSVDTEAPRPAPKYQDVSSEKPAQKQDQGGYGAMRLKRRNWYPSAKENEVKLNESDWE
      10      20      30      40      50      60      70

      80      90     100     110     120     130
ATGLPTKPKELPKRQKSVEIKVETDGDSD---IYSSPYLTSPNHQNGSAGNGVNQPKNQATGHENFQYVY
-----
TTGLPSNPKNLPERQKSVIDQVETDGDSSNNSNIYSSPYLTQSNHQNGNTGNGVNQPKNEVTDYKNFKYVY
      80      90     100     110     120     130     140

      140     150     160     170     180     190     200
SGWIFYKHAASEKDFS-NKKI-KSGDDGYIFYHGEKPSRQLPASGKVIYKGVVWHFVTDTKKGQDFREIIQP
=====
SGWIFYKHAKREVNLAPEPKIAKNGDDGYIFYHKGDPQRQLPASGKITIKGVVWHFATDTKRGQKFREIIQP
      150     160     170     180     190     200     210

      210     220     230     240     250     260     270
SKKQGDRIYSGFGSGDSEESYKNESTLKDDEHGYGFTSNLEVDGNGKLTGKLI RNNASLNNNTNNDKHT
==
SKNQGDRIYSGFGSGDDDEQYSNKNESMLKDGHEGYGFASNLEVDGDKKLTGKLI RNNANQNNTNNDKHT
      220     230     240     250     260     270     280

      280     290     300     310     320     330     340
TQYYSLDAQITGNRFNGTATATDK-KEN-ETKLHPFVSDSSSLSGGFFGPQGEELGFRFLSDDQKVAVVG
=====
TQYYSLDATLKGNRFSGKAEATDKPKNDGETKEHPFVSDSSSLSGGFFGPQGEELGFRFLSNDQKVAVVG
      290     300     310     320     330     340     350

      350     360     370     380     390     400     410
SAKTKDKLENG-AA-ASGSTGAAASGGAAGTSSSENSKLTTVLDAVELTLNDKKIKNLDNFSNAAQLVVDG
=====
SAKTKDKPANGNTAEASGGTDAAASGGAAGTSSSENSKLTTVLDAVELTHGGTAIKNLDNFSNAAQLVVDG
      360     370     380     390     400     410     420

      420     430     440     450     460     470     480
IMIPLLPKDSESGNTQADKGKNGGTEFTRKFEHTPESDKKDAQAGTQTNGAQTASNTAGDTNGKTKTYEV
=====
IMIPLLQNSTGKNNQPDQKNGGTAFIYKTTYTPKNDDKDTKAQTVTGGTQTASNTAGDANGKTKTYEV
      430     440     450     460     470     480     490

      490     500     510     520     530     540     550
EVCCSNLNYLKYGMLTRKNSKSAMQAGGNSSQADAKTEQVEQSMFLOGERTDEKEIPTDQNVVYRGSWYG
=====
EVCCSNLNYLKYGLLTRKTAGNTVGSGNSSPTAAQTD--QSMFLOGERTDENKIPSEQNVVYRGSWYG
      500     510     520     530     540     550

      560     570     580     590     600     610     620
HIANGTSWGSNASDKEGGNRAEFTVNFADKKITGKLTAEENRQAQFTTIEGMIQNGGFEGTAKTAESGFDL
=====
HIASSTSWGSNASDKEGGNRAEFTVNFGEKKITGTLTAENRQEATFTIDGKIEGNGFGSGTAKTAELGFDL
      570     580     590     600     610     620
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630	640	650	660	670	680	690
DQKNTTTRTPKAYITDAKVKGGFYGPKAEELGGWFAYPGDKQTEKATATSSDGNSASSATVVFGAKRQQPVO						
=====						
DQKNTTTRTPKAYITDAKVKGGFYGPKAEELGGWFAYSDDKQTKNATDASGNGNSASSATVVFGAKRQQPVO						
640	650	660	670	680	690	

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Figure 4

	10	20	30	40	50	60	
346		361		380			
1	TKDKLENGAA--ASGSTGAAASGGAAGTSSSENSKLTTVLDAVELTLNDKKIKNLDNFSNA						58
2	TKDKTENGAV--ASGGTDAASNGAAGTSSSENSKLTTVLDAVELKLGDKKEVQKLDNFSNA						58
3	TKDKTENGAV--ASGGTDAASNGAAGTSSSENSKLTTVLDAVELKLGDKKEVQKLDNFSNA						58
4	TQDKPRNGAV--ASGGTGAARSNGAAGQSSENSKLTTVLDAVELTLNDKKIKNLDNFSNA						58
5	TQDKAANGNTAAASGGTDAASNGAAGTSSSENSKLTTVLDAVELTLNDKKIKNLDNFSNA						60
6	KRDKAESGGNGASGGTDAASNGAAGTSSSENSKLTTVLDAVELKSGGKEVKNLDNFSNA						60
7	TKDKPRNGAV--ASGGTDAASNGAAGTSSSENSKLTTVLDAVELTLNDKKIKNLDNFSNA						58
8	TKDKPANGNTAEASGGTDAASGGAAGTSSSENSKLTTVLDAVELTHGGTAIKNLDNFSNA						60
9	TKDKPGNGA---RLQAARCGTSNGAAGQSSENSKLTTVLDAVELKLGDKKEVQKLDNFSNA						57
C	*+DK::*G+:+:*****+*+S+GAAG+SSEN*KLTTVLDAVEL:++*+:++LDNFSNA						

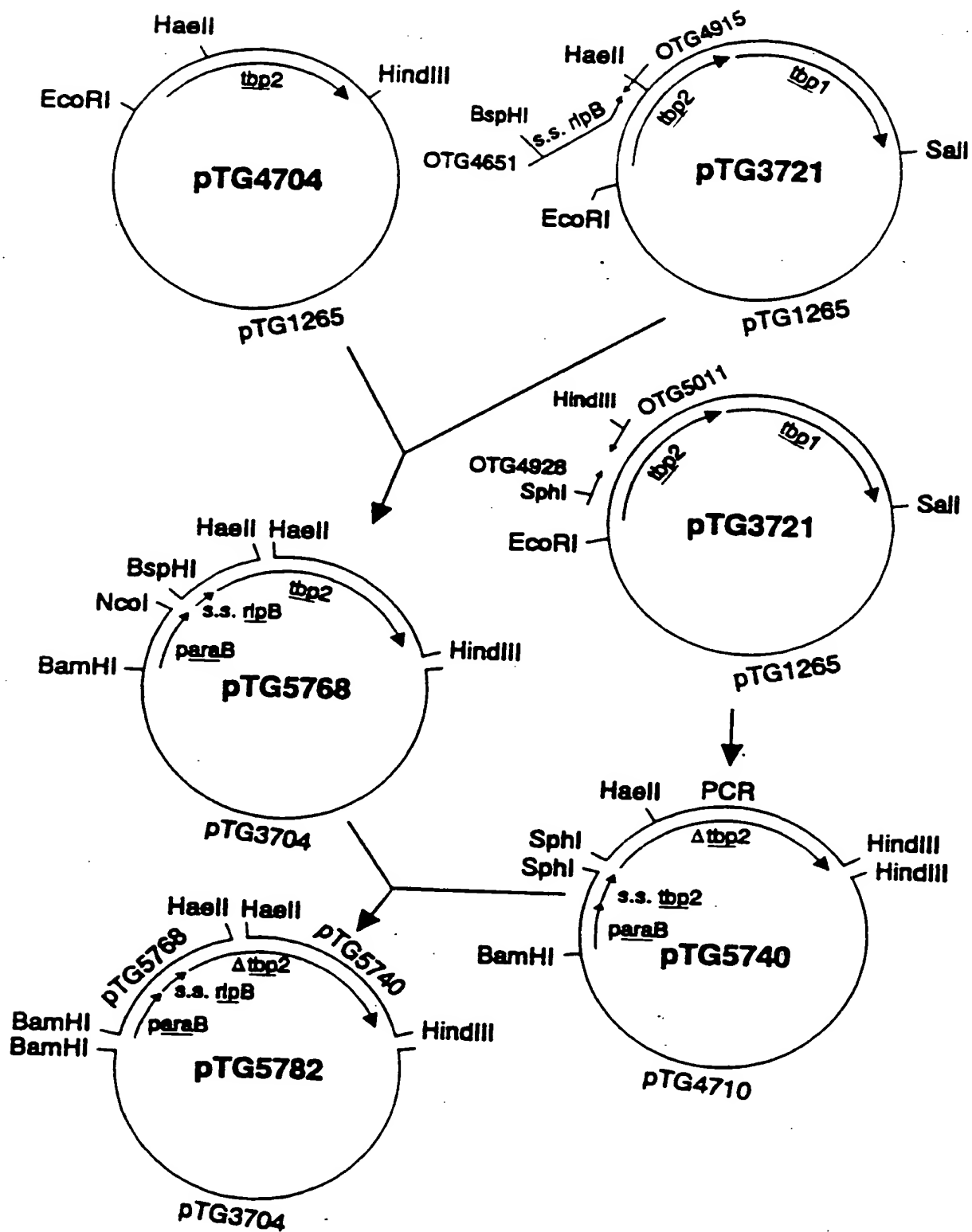
	70	80	90	100	110	120	
	417				445		
1	AQLVVDGIMIPLLPKDSESGNTQADKPK-----NGGTEFTTRKFEHTPESDKKDAQAGTQ						112
2	AQLVVDGIMIPLLPEASESGNNQANQGT-----NGGTAFTTRKFDHTPESDKKDAQAGTQ						112
3	AQLVVDGIMIPLLPEASESGNNQANQGT-----NGGTAFTTRKFDHTPESDKKDAQAGTQ						112
4	AQLVVDGIMIPLLPEASESGKNQANQGT-----NGGTAFTTRKFNETPKSDEKDTQAGTA						112
5	AQLVVDGIMIPLLPETSESGSNQADKKGKNGKNGGGTDFTYKTTYTPKNDDKDTKAQTG						120
6	AQLVVDGIMIPLLPKDSESGNTQADKPK-----NGGTFTRKFEHTPESDKKDAQAGTQ						114
7	AQLVVDGIMIPLLPETSESGNNQADKPK-----NGGTAFTTRKFDHTPKSDEKDTQAGTP						112
8	AQLVVDGIMIPLLPQNSTGKNNQPDQPK-----NGGTAFTTYKTTYTPKNDDKDTKAQTV						114
9	AQLVVDGIMIPLLPKDSESGKNQADKPK-----NGETEFTTRKFEHTPESDEKDAQAGTP						111
C	AQLVV*GIMIP*L:P:.S***+*Q*+:G: NG*T:F*+K*+.TP:+D:KD:+A+T:						

	130	140	150	160	170	180	
	465		482		499		
1	TNGAQTASNTAGDTNGKT-----KTYEVEVCCSNLNYLKYGMLTRKNKSKSAMQAGGNSSQ						167
2	TNGAQTASNTAGDTNGKT-----KTYEVEVCCSNLNYLKYGMLTRKNKSKSAMQAGESSQ						167
3	ANGAQTASNTAGDTNGKT-----KTYEVEVCCSNLNYLKYGMLTRKNKSKSAMQAGESSQ						167
4	ENGNPAASNTAGDANGKT-----KTYEVEVCCSNLNYLKYGMLTRKNKSKSAMQAGESSQ						167
5	AAGSSGAQTDLGKADVNGGKAEKTYEVEVCCSNLNYLKYGMLTRKNKSKSAMQAGGNSSQ						180
6	TNGAQTASNTAGDTNGKT-----KTYEVEVCCSNLNYLKYGLLTRKTAGNTGEGGNGSQT						169
7	TNGAQTASGTAGVTGGQAG-----KTYAVEVCCSNLNYLKYGLLTRKTADNTVGSGNGSST						168
8	TGGTQTASNTAGDANGKT-----KTYEVEVCCSNLNYLKYGLLTRKTAGNTVGSGNGSSPT						169
9	SNGAQTASNTAGDTNGKT-----KTYEVNLC-SNLNYLKYGLLTRKTAGNTGEGGNGSSPT						165
C	:G+++A***G+++++. KTY*V**C*SNLNYLKYG:LTRK:::G::S+:						

	190	200	210	
	521			
1	ADAKTEQVEQSMFLOGERTDEKEIPTDQ-NVV			198
2	ADAKTEQVEQSMFLOGERTDEKEIPSEQ-NIV			198
3	ADAKTEQVGQSMFLOGERTDEKEIPSEQ-NIV			198
4	ADAKTEQVGQSMFLOGERTDEKEIPNDQ-NVV			198
5	ADAKTEQVEQSMFLOGERTDEKEIPNDQ-NVV			211
6	AAAQTAQGAQSMFLOGERTDEKEIPSEQ-NVV			200
7	AAAQTAQGAQSMFLOGERTDEKEIPKEQQDIV			200
8	AAAQTD--AQSMFLOGERTDENKIPSEQ-NVV			198
9	AA-QTAQGAQSMFLOGERTDEKEIPNDQ-NVV			195
C	A:::T:::QSMFLOGERTDE**IP::Q *+V			

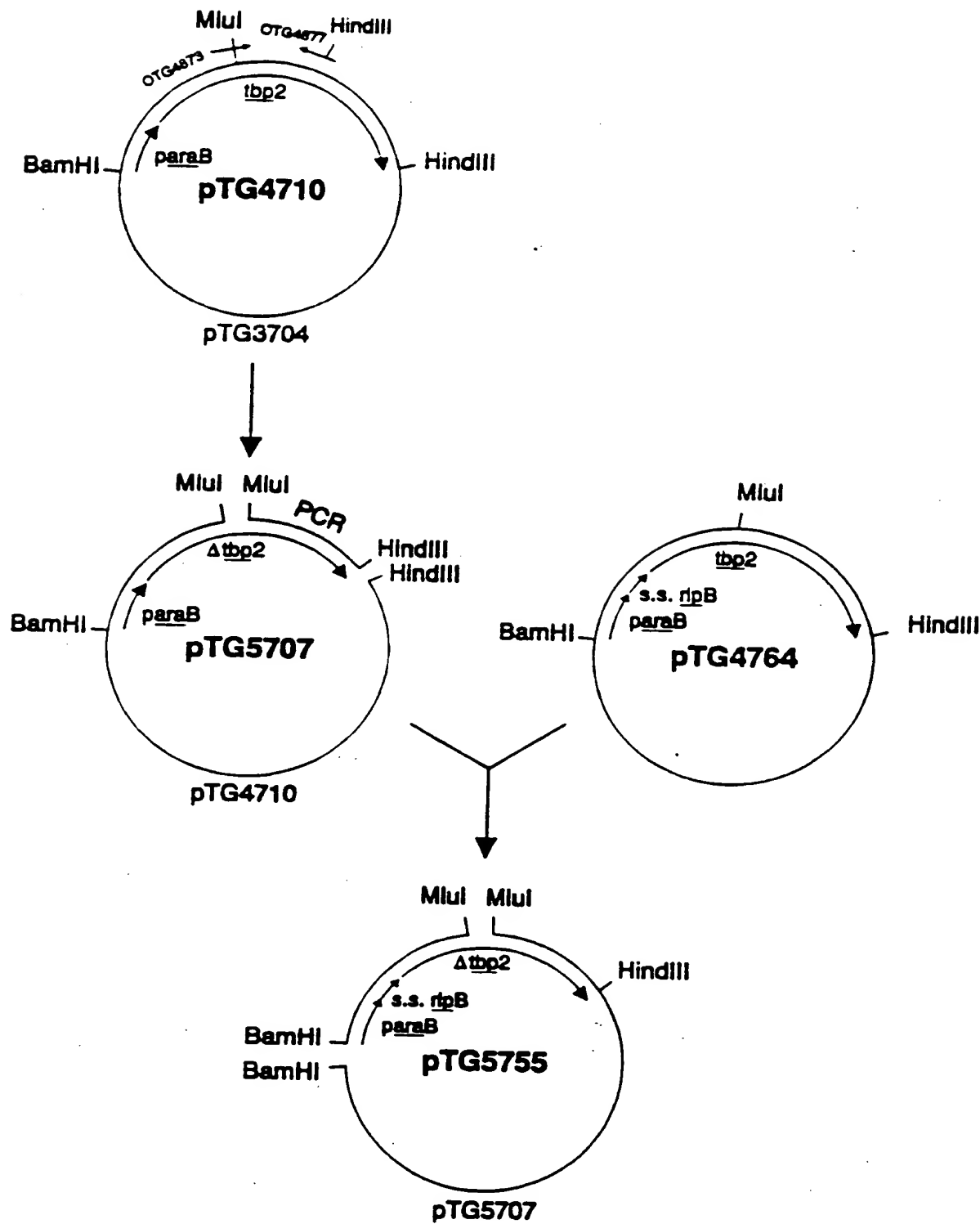
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Figure 5



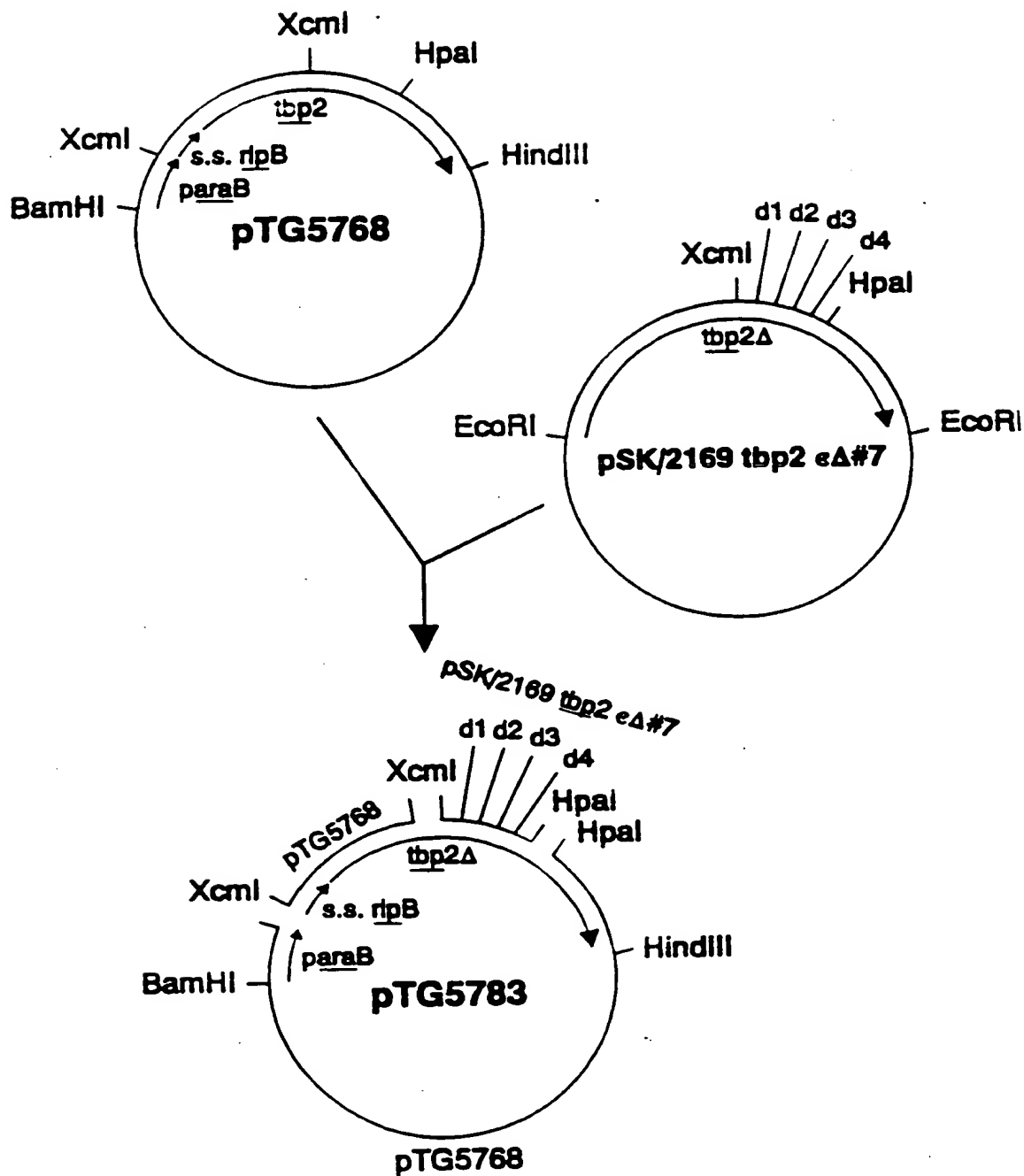
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Figure 6



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Figure 7



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Figure 8

M982

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BZ83

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      10      20      30      40      50      60      70
CLGGGGSFDLDSVDTEAPRPAPKYQDVSSSEKPAQAKDQGGYGFMRLKRRNWYPGAESEVKLNESDWEA
=====
CLGGGGSFDLDSVDTEAPRPAPKYQDVSSSETPQAQKDQGGYGFMRFKRRNWYPKNEEDHKALSEADWEK
      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
TGLPTKPKELPKRQKSVIEKVETDGDSDIYSSPYLTPSNHQNGSAGNGVNPKNQATGHENFQYVYSGWF
= - - - - - = - - - - - = - - - - - = - - - - - = - - - - - = - - - - - = - - - - -
LG AGKPDEFPORNE ILN M TDG  ILSES L  QL GE G G  KSRVEGYTDFQYVRSGYI
      80      90     100     110     120

      150     160     170     180     190     200     210
YKHAASEKDFSNNKKIKSGDDGYIFYHGEKPSRQLPASGKVIYKGVWHFVTDTKKGQDFREIIQPSKKQGD
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
YRNGANKIDFQKKIALSGPDGYLFYKGSNPSQALPM GKVGYKGTWDYVTDAKMGQKFSQL AGFPAGD
      130     140     150     160     170     180

      220     230     240     250     260     270     280
RYSGFSGDGSSEEYSNNKNESTLKDDHEGYGFTSNLEVDFGNKKLTGKLI RNNASLNNNTNNDKHTTQYYSL
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
RYGALSAAEEADVLRNKSEA  QQGQTDGFLTSEFEVDFAAKTMTGALYRNNRITNNETENKAKQIKRYDI
      200     210     220     230     240     250

      290     300     310     320     330     340
DAQITGNRFGTATATDK KENETKLHPFVSDSSSLSGGFFGPGQGEELGFRFLSDDQKVAVVGSAKTKDK
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
QADLHG NRFS GKATATDKPKNDETKEHPFVSDSSSLSGGFFGPKGEELGFRFLSDDQKVAVVGSAKTKDK
      260     270     280     290     300     310     320

      360     370     380     390     400     410
LENGAAASGSTGAAASGGAAGTSSSENSKLTTVLDAVELTLNDKKIKNLDNFSNAAQLVVDGIMIPLLPKD
=====
LENGAAASGSTGAAASGGAADMPSENGKLTTVLDAVELKSGGKEVKNLDNFSNAAQLVVDGIMIPLLPKN
      330     340     350     360     370     380     390

      430     440     450     460     470     480
SESGNTQADKGKNGGTEFTRKFEHTPESDKKDAQAGTQTNGAQTASNTAGDTNGKTKTYEVEVCCSNLNY
=====
SESESNQADKGKNGGTAFTTRKFEHTPESDKKDTQAGTAENG NPAASNTAGDTNGKTKTYEVEVCCSNLNY
      400     410     420     430     440     450     460

      500     510     520     530     540     550
LKYGMLTRKNSKSAMQAGGNSSQADAKTEQVEQSMFLOGERTDEKEIPTDQ NVVYRGSWYGHIANGTSW
=====
LKYGMLTRKNSKSAMQAGENGSLADAKTEQVEQSMFLOGERTDEKEIPKEQQDIVYRGSWYGHIANDTSW
      470     480     490     500     510     520     530

      570     580     590     600     610     620
SGNASDKEGGNRAEFTVNFADKKITGKLTAE NRQAQFTTIEGMIQNGFEGTAKTAESGFDLDQKNTTTRT
=====
SGNASDREGGNRADFTVNFGTKKINGTLTAE NRQEATFTIVGDIKDNGFEGTAKTADSGFDLDQSNTTTRT
      540     550     560     570     580     590     600
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	640	650	660	670	680	690
	PKAYITDAKVKGGFYGP	KAEELGGWFAYPGDKQTEKATATSSDGNSASSATVVFGAKRQOPVQ				
	=====					
	PKAYITDAKVKGGFYGP	KAEELGGWFAYPGDKQTEKATVTSGDGLSASSATVVFGAKRQKPVO				
610	620	630	640	650	660	

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Figure 9

M982

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BZ163

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      10      20      30      40      50      60
CLGGGGSFDLDSVDTEAPRPAP KYQDVSSEKPPQAQKDQGGYGFMRLKRRNWYPGAESEVKLNESDWE
=====
CLGGGGSFDLDSVDTEAPRPAPPKYQDVSSEKPPQAQKDQGGYGFMRLKRRNRHPQAKEDKVELNPNDWE
      10      20      30      40      50      60      70

      80      90     100     110     120     130
ATGLPTKPKELPKRQKSVIEKVETDGDSDIYSSPYLTSPSNHQNGSAGNGVNQPKNQATGHENFQYVYSGW
=====
ETGLPSKPQNLPERQQSVIDKVKTDDGSNIYTSPLYTQSNHQNGSTNSGANQPKNEVKDYKNFKYVYSGW
      80      90     100     110     120     130     140

      150     160     170     180     190     200
FYKHAASEKDFSNKKIKSGDDGYIFYHGEKPSRQLPASGKVIYKGVWHFVTDTKKGQDFREIIQPSKKQG
=====
FYKHAESEREFSSKIKFKSGDDGYIFYHGKDPQRQLPTSEKVIYKGVWHFVTDTEKGQKFNDILETSKGQG
      150     160     170     180     190     200     210

      220     230     240     250     260     270
DRYSGFGSGDGSEESYNNKNESTLKDDHEGYGFTSNLEVDVFGNKKLTGKLI RNNASLNNNTNNDKHTTQYYS
=====
DRYSGFGSGDDGETTSNRDTSNLDKHEGYGFTSNLEVDVFGSKKLTGKLI RNN RVTNATTNDKYTTQYYS
      220     230     240     250     260     270

      290     300     310     320     330     340
LDAQITGNRFRNGTATATDKKENE TKLHPFVSDSSSLSGGFFGPQGEELGFRFLSDDQKVAVVGSAKTKD
=====
LDAQITGNRFRNGKAIAADKPDGTTGKLHPFVSDSSSLSGGFFGPKGEELGFRFLSDDKKVAVVGSAKTKD
      290     300     310     320     330     340

      360     370     380     390     400     410
KLENGAAASGSTGAAASGGAAGTSSSENSKLTTVLDAVELTLNDKKIKNLDNFSNAAQLVVDGIMIPLLPK
=====
KTENGAVASGGTDAAASNGAAGTSSSENSKLTTVLDAVELKLGDKEVQKLDNFSNAAQLVVDGIMIPLLPE
      360     370     380     390     400     410

      430     440     450     460     470     480
DSESGNTQADKGNKGTEFTRKFEHTPESDKKDAQAGTQTNGAQTASNTAGDTNGKTKTYEVEVCCSNLN
=====
TSESGNNQANQGTNGGTAFTTRKFDHTPESDKKDAQAGTQTNGAQTASNTAGDTNGKTKTYEVEVCCSNLN
      430     440     450     460     470     480

      500     510     520     530     540     550
YLKYGMLTRKNKSKSAMQAGGNSSQADAKTEQVEQSMFLOGERTDEKEIPTDQNVVYRGSWYGHIANGTSW
=====
YLKYGMLTRKNKSKSAMQAGESSSQADAKTEQVGQSMFLOGERTDEKEIPSEQNIVYRGSWYGHIASSTSW
      500     510     520     530     540     550

      570     580     590     600     610     620
SGNASDKEGGNRAEFTVNFADKKITGKLTAE NRQAQTFTIEGMIQNGGFEGTAKTAESGFDLDQKNTTRT
=====
SGNASDKEGGNRAEFTVNFGEKKITGTLTAENRQEATFTIDGKIEGNGFSGTAKTAELGFDLDQKNTTRT
      570     580     590     600     610     620
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640	650	660	670	680	690
PKAYITDAKVKGGFYGP	KAEELGGWFAYPGDKQ	TEKATATSSD	GNSASSATVV	FGAKRQ	QPVQ
=====					
PKAYITDAKVQGGFYGP	KAEELGGWFAYQGD	KQTENTTVAS	GNGNSASSATVV	FGAKRQ	KPVQ
640	650	660	670	680	690

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Figure 10

	10	20	30	40	50	60	
	346	361	380				
1	TKDKLENG--AAASGSTGAAASGGAAGTSSSENSKLT	TTVLDAVELT	LN	DKKI	KN	LDNFSN	57
2	TKDKTENG--AVASGGTDAASNGAAGTSSSENSKLT	TTVLDAVELK	LG	DKEV	QK	LDNFSN	57
3	TQDKPRNG--AVASGGTGAARSNGAAGQSSSENSKLT	TTVLDAVELT	LN	DKKI	KN	LDNFSN	57
4	TKDNTANGNTAAASGGTDAASNGAAGTSSSENSKLT	TTVLDAVELT	LN	DKKI	KN	LDNFSN	60
5	TKDKTENG--AVASGGTDAASNGAAGTSSSENSKLT	TTVLDAVELK	LG	DKEV	QK	LDNFSN	57
6	TQDKAANGNTAAASGGTDAASNGAAGTSSSENSKLT	TTVLDAVELT	LN	DKKI	KN	LDNFSN	59
7	RKDKAESGGGNGASGGTDAASNGAAGTSSSENSKLT	TTVLDAVELK	SGG	KEV	QK	LDNFSN	59
8	TKDKPANGNTAEASGGTDAASGGAAGTSSSENSKLT	TTVLDAVELT	HG	GTAI	KN	LDNFSN	59
9	TKDKPRNG--AVASGGTDAASNGAAGTSSSENSKLT	TTVLDAVELT	LN	DKKI	KN	LDNFSN	57
10	TKDKLENG--AAASGSTGAAASGGAADMPSENGKLT	TTVLDAVELK	SGG	KEV	QK	LDNFSN	57
11	TKDKTENG--AVASGGTDAASNGAAGTSSSENSKLT	TTVLDAVELK	LG	DKEV	QK	LDNFSN	57
C	**D...*G...:ASG*T+AA*S+GAA***SEN+KLTTVLDAVEL:++*::++LDNFSN						
	70	80	90	100	110	120	
	417				445		
1	AAQLVVDGIMIPLLPKDSESGNTQADKGGK-----	NGGTEFTRKFEHT	PESDKK	DAQAGT		111	
2	AAQLVVDGIMIPLLPEASESGNNQANQGT-----	NGGTAFTRKFDHT	PESDKK	DAQAGT		111	
3	AAQLVVDGIMIPLLPEASESGNNQANQGT-----	NGGTAFTRKFNET	PKSDEK	DTQAGT		111	
4	AAQLVVDGIMIPLLPEASESGNNQANQGT-----	NGGTAFTRKFAHT	PKSDEK	DTQAGT		114	
5	AAQLVVDGIMIPLLPEASESGNNQANQGT-----	NGGTAFTRKFDHT	PESDKK	DAQAGT		111	
6	AAQLVVDGIMIPLLPETSESGSNQADKGGKGGKNGKNGG	TDFTYKTTYTPK	NDDK	DTKAQT		119	
7	AAQLVVDGIMIPLLPKDSESGNTQADKGGK-----	NGGTFTRKFEHT	PESDKK	DAQAGT		113	
8	AAQLVVDGIMIPLLPQNSTGKNNQPDQGGK-----	NGGTAFIYKTTYTP	KNDK	DTKAQT		113	
9	AAQLVVDGIMIPLLPETSESGNNQADKGGK-----	NGGTAFTRKFDHT	PKSDEK	DTQAGT		111	
10	AAQLVVDGIMIPLLPKNSESESNQADKGGK-----	NGGTAFTRKFEHT	PESDKK	DTQAGT		111	
11	AAQLVVDGIMIPLLPETSESGNNQANQGT-----	NGGTAFTRKFDHT	PESDKK	DAQAGT		111	
C	AAQLVV*GIMIP*P+.S***+*Q*::G: NGGT+F**K*.*TP:*D:KD:+A*T						
	130	140	150	160	170	180	
	465		482		499		
1	QTNGAQTASNTAGDTNG-----	KTKTYEVEVCCSNL	NYLKYGMLTRKNSKSAMQAGGNS		166		
2	QANGAQTASNTAGDTNG-----	KTKTYEVEVCCSNL	NYLKYGMLTRKNSKSAMQAGESS		166		
3	AENGNPAAASNTAGDANG-----	KTKTYEVEVCCSNL	NYLKYGMLTRKNSKSAMQAGESS		166		
4	AANGDQAASNTAGDTNG-----	KTKTYEVEVCCSNL	NYLKYGLLTRKTAGNTGEGGNGSQ		169		
5	QTNGAQTASNTAGDTNG-----	KTKTYEVEVCCSNL	NYLKYGMLTRKNSKSAMQAGESS		166		
6	GAAGSSGAQTDLGRADVNGGKAETKTYEVEVCCSNL	NYLKYGMLTRKNSKSAMQAGGNS		179			
7	QTNGAQTASNTAGDTNG-----	KTKTYEVEVCCSNL	NYLKYGLLTRKTAGNTGEGGNGSQ		168		
8	VTGGTQTASNTAGDANG-----	KTKTYEVEVCCSNL	NYLKYGLLTRKTAGNTVGSGNSP		168		
9	PTNGAQTASGTAGVTGGQAG----	KTYAVEVCCSNL	NYLKYGLLTRKTADNTVGSGNGSS		167		
10	AENGNPAAASNTAGDTNG-----	KTKTYEVEVCCSNL	NYLKYGMLTRKNSKSAMQAGENG		166		
11	QTNGAQTASNTAGDTNG-----	KTKTYEVEVCCSNL	NYLKYGMLTRKNSKSAMQAGESS		166		
C	:::G:++A****G****. :+KTY*VEVCCSNLNYLKYG+LTRK++++++G::**						

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Figure 10 (continuation)

	190	200	210	
	521			
1	QADAKTEQVEQSMFLOGERTDEKEIPTDQ-NVV			198
2	QADAKTEQVGQSMFLOGERTDEKEIPSEQ-NIV			198
3	QADAKTEQVGQSMFLOGERTDEKEIPNDQ-NVV			198
4	TAAAQTAQGAQSMFLOGERTDEKEIPSEQ-NV-			200
5	QADAKTEQVEQSMFLOGERTDEKEIPSEQ-NIV			198
6	QADAKTEQVEQSMFLOGERTDEKEIPNDQ-NV-			210
7	TAAAQTAQGAQSMFLOGERTDEKEIPSEQ-NV-			199
8	TAAAQT--DAQSMFLOGERTDENKIPSEQ-NVV			198
9	TAAAQTAQGAQSMFLOGERTDEKEIPKEQQDIV			200
10	LADAKTEQVEQSMFLOGERTDEKEIPKEQQDIV			199
11	QADAKTEQVGQSMFLOGERTDEKEIPSEQ-NIV			198
C	:A+A+T+++.QSMFLOGERTDE**IP:+Q *:+			